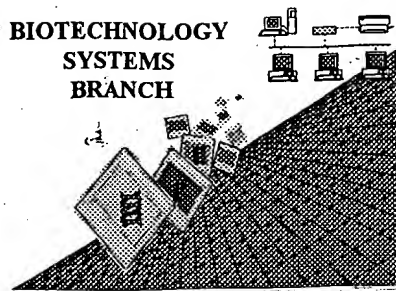


RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/942,336
Source: O/PK
Date Processed by STIC: 9/18/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/942,336
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 _____ Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 _____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 _____ Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 _____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 _____ Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 _____ PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 _____ Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 _____ Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 _____ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 _____ Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 _____ Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 _____ PatentIn-2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 _____ Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	

OIPE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/942,336

DATE: 09/18/2001
 TIME: 11:34:12

Input Set : A:\P02039US1.txt
 Output Set: N:\CRF3\09182001\I942336.raw

**Does Not Comply
 Corrected Diskette Needed**

pg 1-2

OK

3 <110> APPLICANT: Ashizawa, Tetsuo
 4 Tohru, Matsuura
 6 <120> TITLE OF INVENTION: DNA TEST FOR SCA-10
 8 <130> FILE REFERENCE: P02039US1/10023139/OTA01-01
 10 <140> CURRENT APPLICATION NUMBER: US/09/942,336
 11 <141> CURRENT FILING DATE: 2001-08-29
 13 <150> PRIOR APPLICATION NUMBER: US 60/229,406
 14 <151> PRIOR FILING DATE: 2000-08-31
 16 <160> NUMBER OF SEQ ID NOS: 13
 18 <170> SOFTWARE: PatentIn version 3.0

ERRORED SEQUENCES

338 <210> SEQ ID NO: 13
 339 <211> LENGTH: 45
 340 <212> TYPE: DNA
 341 <213> ORGANISM: Mus musculus
 343 <220> FEATURE:
 344 <221> NAME/KEY: misc_feature
 345 <222> LOCATION: (1)..(45)
 347 <400> SEQUENCE: 13
 348 cactgcagag atgagagggtc cgtgagatgg aatctgaatg tgttc
 E--> 350 25067696.1 1

45

delete at end of file

see next page

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/942,336

DATE: 10/17/2001

TIME: 10:29:16

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\10172001\I942336.raw

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155 acgagtgatg agccactcac caaggatgac atccctgtgt ttttgcggca tgctgagttg 1020
157 attgcaagca cctttgtgga tcagtgcag actgtgctca agctggcctc tgaggagcct 1080
159 cctgatgatg aggaggcact ggctacaatt aggtttctcg acgtcctgtg cgaaatgact 1140
161 gtgaatactg agctgctcgg ctatctgcag gttttccctg gcttgctgga aagagtgatt 1200
163 gatcttttgc ggggtgattca tgtagctgga aaagaaacca caaacatctt cagtaattgt 1260
165 ggttgctgga gagcagaagg tgacatctcc aatgtggcca atgggtttaa gtctcatctc 1320
167 attcgtctga ttggaaatct gtgttacaag aataaagata accaagacaa ggtaaatgag 1380
169 ctggatggtg tcccgttgat cctggacaac tgcaacatca gtgacagtaa cccctttctg 1440
171 acccagtggg tgatatatgc catccgaaac cttaccgaag acaacagcca aaaccaagat 1500
173 ttgattgcaa agatggagga acaggggctg gcagatgcac ccctacttaa aaaagtgggt 1560
175 ttgaagtgtg aaaagaaagg cgaaaagctg atcctgaaat ctactagaga caccctaag 1620
177 ccatgaatga actacatcca aatacctgaa tttttggaat ctgtttcatg gatttttcat 1680
179 cttctaccgt atgtgaaatt gcaagtgttt gaagatttat aagtacaaat ttgggaacat 1740
181 acaaatcttt taggtagtag agtttaacgt gtataagcta aaagtgaag taactgagtg 1800
183 ttctcttggt tctttgcatt aatgtaactg tgtggtttgc ctttgtcccc ctggatagaa 1860
185 cgtgcattta aagaatatat tgtacttact gtgacagcag ataataaacc agtctcttgg 1920
187 agggcaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 1971
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190 <210> SEQ ID NO: 3

191 <211> LENGTH: 21

192 <212> TYPE: DNA

193 <213> ORGANISM: PRIMERS

195 <220> FEATURE:

196 <221> NAME/KEY: misc_feature

197 <222> LOCATION: (1)..(21)

198 <223> OTHER INFORMATION: Primers

201 <400> SEQUENCE: 3

202 agaaaacaga tggcagaatg a

21

205 <210> SEQ ID NO: 4

206 <211> LENGTH: 20

207 <212> TYPE: DNA

208 <213> ORGANISM: PRIMERS

210 <220> FEATURE:

211 <221> NAME/KEY: misc_feature

212 <222> LOCATION: (1)..(20)

213 <223> OTHER INFORMATION: Primers

216 <400> SEQUENCE: 4

217 gcctgggcaa catagagaga

20

220 <210> SEQ ID NO: 5

221 <211> LENGTH: 197

222 <212> TYPE: DNA

223 <213> ORGANISM: HUMAN

225 <400> SEQUENCE: 5

226 agaaaacaga tggcagaatg ataaactcaa tcatgttgat aaatatatta aatgtaaagt 60

228 gcttaaatat ccaactaaaa gactactaga atggattcta ttctattcta ttctattcra 120

230 ttcraattcta ttctattcta ttctattcta ttctattcta ttctttttga gatgaagtct 180

232 ctctatgttg cccaggc 197

235 <210> SEQ ID NO: 6

236 <211> LENGTH: 20

237 <212> TYPE: DNA

see item 10 on Env Summary Sheet

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/942,336

DATE: 09/18/2001

TIME: 11:34:13

Input Set : A:\P02039US1.txt

Output Set: N:\CRF3\09182001\I942336.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number

L:350 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:46 SEQ:13

L:350 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:9

L:350 M:252 E: No. of Seq. differs, <211>LENGTH:Input:45 Found:46 SEQ:13